

ID 86

## Molecular variability and genetic relationships of *Sporisorium scitamineum* isolates, the causal organism of sugarcane smut disease of Sri Lanka

A.N.W. Sumedha Thushari<sup>1\*</sup> and D.M. De Costa<sup>2</sup>

<sup>1</sup> Division of Crop Protection, Sugarcane Research Institute, Uda Walawe, Sri Lanka

<sup>2</sup> Department of Agricultural Biology, Faculty of Agriculture, University of Peradeniya, Peradeniya, Sri Lanka

### Abstract

Sugarcane smut caused by *Sporisorium scitamineum* is a devastating disease of sugarcane. Production of smut-resistant varieties is one of the major objectives in sugarcane breeding programs in almost all sugarcane-producing countries including Sri Lanka. Since no adequate scientific information is available, this research was aimed to get an insight on the genetic variability of sugarcane smut pathogen in Sri Lanka in order to support an effective breeding program for sugarcane smut disease. The genetic diversity of 83 *Sporisorium scitamineum* isolates was comprehensively evaluated in this study. The isolates were collected from 15 different sugarcane varieties that were grown in seven major sugarcane growing areas of Sri Lanka. Genomic DNA extracted from the fungal colonies originating from diploid teliospores were subjected to PCR using bE4 and bE8 specific primers and ITS 4 as well as ITS 1 universal primers. PCR products were sequenced. Sequence results using both primers showed 99% sequence similarity among the isolates. Using 16 ISSR primers, we used the inter-simple sequence repeat (ISSR) polymorphism molecular marker approach. The ISSR primers produced 104 amplified DNA fragments that are 100% polymorphic. The polymorphic information content (PIC) values ranged from 0.25 to 0.46 with an average of 0.37, indicating that the collected isolates exhibit a moderate degree of genetic diversity. Genetic differentiation coefficient ( $G_{st}$ ) was estimated to be 0.241, meaning that only 24% of the total genetic variation originates between populations, while 76% originates within populations. Gene-flow ( $Nm$ ) was calculated as 1.572, indicating that gene flow across populations occurs at a faster rate. The collected isolates clustered into five genetically distinct groups which did not correspond to their geographical origin. The result of this study suggests that considerable genetic variation exist among isolates collected from major sugarcane growing areas in Sri Lanka. Therefore, it is suggested to use a mixture of sugarcane smut isolates collected from all sugarcane growing areas when screening for smut-resistant sugarcane varieties for the industry in Sri Lanka to address different adoptive potentials of the isolates.

**Keywords:** Genetic relationship, Inter-simple sequence repeats, Sugarcane, Smut

\*Corresponding Author: [asumedhathushari@yahoo.com](mailto:asumedhathushari@yahoo.com)